AMENDMENTS TO THE SPECIFICATION

Please amend the specification as follows:

1) On page 25, line 17, please delete "LeadQuest® library" and replace with "LEADQUEST® , library of screening compounds".

Compounds which can be evaluated include, but are not limited to: drugs; toxins; proteins; polypeptides; peptides; amino acids; antigens; cells, cell nuclei, organelles, portions of cell membranes; viruses; receptors; modulators of receptors (e.g., agonists, antagonists, and the like); enzymes; enzyme modulators (e.g., such as inhibitors, cofactors, and the like); enzyme substrates; hormones; nucleic acids (e.g., such as oligonucleotides; polynucleotides; genes, cDNAs; RNA; antisense molecules, ribozymes, aptamers), and combinations thereof. Compounds also can be obtained from synthetic libraries from drug companies and other commercially available sources known in the art (e.g., including, but not limited, to the ~~LeadQuest® library~~ LEADQUEST® , library of screening compounds) or can be generated through combinatorial synthesis using methods well known in the art. In one aspect, a compound is identified as a modulating agent if it alters the site of modification of a polypeptide and/or if it alters the amount of modification by an amount that is significantly different from the amount observed in a control cell (e.g., not treated with compound) (setting p values to < 0.05). In another aspect, a compound is identified as a modulating agent, if it alters the amount of the polypeptide (whether modified or not).

2) On page 18, lines 22-23, please delete "available at http://www-genome.wi.mit.edu/SNP/human/index.html" and replace with "retrieved from http://www-genome.wi.mit.edu/SNP/human/index.html [on-line, retrieved on 2004-02-17]".

In one preferred aspect, peptide internal standards corresponding to proteins expressed from nucleic acids comprising single nucleotide polymorphisms are synthesized to identify variant proteins encoded by such nucleic acids. Thus, peptide internal standards can be generated corresponding to SNP's which map to coding regions of genes and can be used to identify and quantify variant protein sequences on an individual or population level. SNP sequences can be accessed through The Human SNP database ~~available at~~

~~http://www-genome.wi.mit.edu/SNP/human/index.html~~ retrieved from http://www-genome.wi.mit.edu/SNP/human/index.html [on-line, retrieved on 2004-02-17].